physiological community profile

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Introduction

In recent years, small- and mid-scale biogas plants have thrived in Europe and led to a change in land-use. Manures that used to be applied to agricultural soils are now used for energy generation in biogas reactors and instead digestate is applied to agricultural soils. Here we present the results of a study simulating soil amendment with either anaerobically digested or fresh cattle manure and its effect on the microbial community.

Aims

-Investigate the resistance and resilience of the resident microbiota
-Detect differences in the microbial biomass and activity after fertilizer amendment
-Elucidate discrepancies of the physiological community profile

Methodology

In a microcosm experiment (Fig.1) we applied a single amendment of either treatment to agricultural soil (non-sterilized or sterilized by gamma-irradiation), equal to 80 kg N ha^{-1}. The effect of amendments on the community structure was tested immediately and after 1 and 3 months by PCR-DGGE (primer pairs: bacteria: 984f-GC/1378r[1]; fungi: FF1-GC/F390r[2]; archaea: (nested PCR: A109F/934r[3] and 357F-GC/693R[4]), CLPP through MicroResp™ (6 sugars, 5 amino acids, 4 carboxylic acids) and measurement of basal respiration, microbial biomass and the metabolic quotient through IRGA and SIR.

Figure 1: Microcosm experiment with soil columns, filled either with non-sterile or sterilized (St) soil and incubated for 0m, 1m and 3m. Amendment either with fresh manure (M) or digestate (S) and unamended control (C)

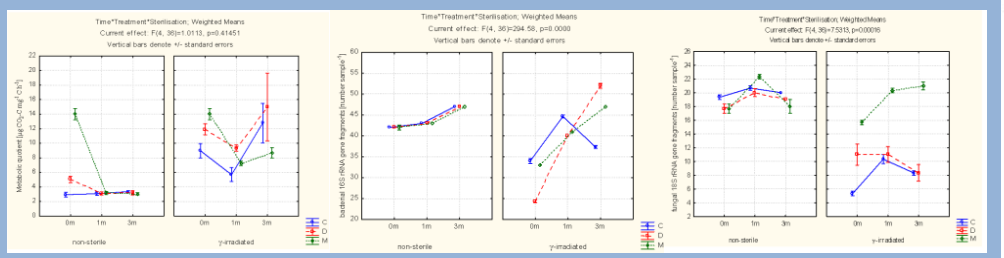

Figure 2: (left) evolution of the metabolic quotient [µg CO_2-C mg^{-1} C h^{-1}] (middle) bacterial 16S rRNA gene fragments $sample^{-1}$ (DGGE) and (right) fungal 18S rRNA gene fragments $sample^{-1}$ over time; C, D, M refer to control, digestate (anaerobically digested cattle manure and fresh cattle manure, respectively.

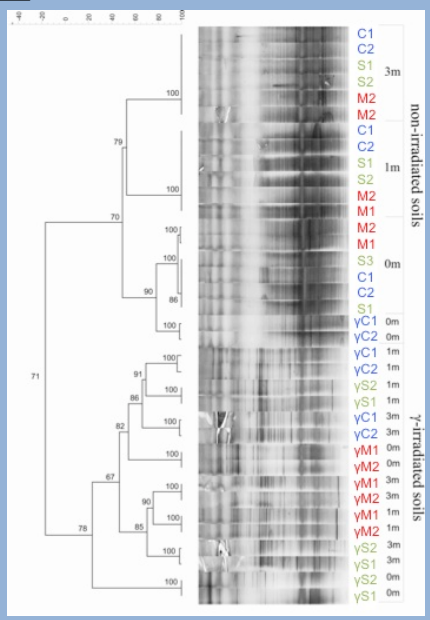

Figure 3: Cluster analysis of bacterial DGGE fingerprints. Values at the branches indicate the percentage of similarity (Dice correlation coefficient).

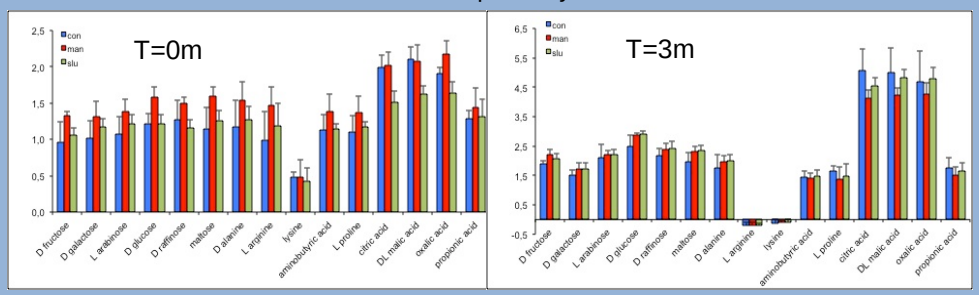

Figure 4: Normalized substrate utilization for non-sterile microcosms at time point 0m and 3m (1m showed nearly equal results to time point 3m)

Results and Discussion

The community structure of dominant fungi and bacteria was not affected by either amendment, indicating the ability of the indigenous microbiota to outcompete allochthonous microorganisms (Fig.2 (middle and right), Fig3). Influence of amendment on the microbial community structure was higher for archaea. Soil microbial biomass was not changed, whereas basal respiration was significantly higher after amendment (Fig.2 (left)), especially when using fresh manure. CLPP revealed initially higher substrate utilization (especially sugars) and a generally reduced utilization of lysine and amino-butyric acid after 1m (similar to 3m) (Fig. 4). Differences were more pronounced for manure application (0m), but both treatments returned to control levels for all parameters after 1m.

In conclusion, amendment with anaerobically digested manure did not have a greater impact on soil microbial parameters than fresh manure

[1]Vainio et al. Mycol. Research (2000) 104:927-936; [1]Nüberl et al. Appl. Env. Microbiol. (1999) 65:422-430; [2]Heuer et al. Appl. Envir. Microbiol (1997) 63:3233-3241; [3]Grosskopf et al. Appl. Envir. Microbiol (1998) 64:960-969; [4] Yu et al. Appl. Envir. Microbiol (2008) 74:889-893.